Once you have obtained your DNA sequence, follow the basic bioinformatics procedure below to identify your microalga and learn a little about it.

2. Under the "Basic BLAST" section, click on the "nucleotide blast" link.
3. Copy and paste your sequence into the query sequence box.
4. Expand the "Algorithm Parameters" section by clicking on the + sign.
5. Change the sequences returned from 100 to 10 on the "Max target sequences" dropdown menu.
6. Check the "Show results in a new window" box then, click the "BLAST" button.

Look at the top header of your results. How many nucleotides long is your sequence?

7. Look at the "Descriptions" section and find the first result (hit).

   What is the genus and species of the organism for this hit?

   What is the name of the gene?

   What is the accession number?

   What is the E value and Query coverage?

8. At the top of the "Descriptions" section, select All sequences, then select "Distance tree of results".

   What organism is the nearest neighbor on the tree?

   Is this same organism shown as the first BLAST hit?

9. Close the tree tab.

10. Click on the Accession/Sequence ID number of the first BLAST hit.

   Are there any publications associated with this sequence?

11. Copy and paste the genus and species of the organism into the box at the top of the page and select "Taxonomy" from the dropdown menu on the left.

   To which group of algae does this organism belong?